

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: BAYLOR COLLEGE OF MEDICINE
SMITH, JAMES R.

(ii) TITLE OF INVENTION: SENESCENT CELL DERIVED
INHIBITORS OF DNA SYNTHESIS

10

(iii) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: HOWREY & SIMON
(B) STREET: 1299 PENNSYLVANIA AVENUE, N.W.
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(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20004

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
30 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/808,523
(B) FILING DATE: 16-DEC-1991

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/970,462
(B) FILING DATE: 02-NOV-1992

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/113,372
(B) FILING DATE: 30-AUG-1993

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TOGETHER

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/153,564
(B) FILING DATE: 17-NOV-1993

5 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/203,535
(B) FILING DATE: 25-FEB-1994

10 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/229,420
(B) FILING DATE: 15-APR-1994

15 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/274,535
(B) FILING DATE: 13-JUL-1994

20 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT US94/09700
(B) FILING DATE: 26-AUG-1994

25 (viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: 225-102-CIP9

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30 (2) INFORMATION FOR SEQ ID NO:1:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

1000000-1000000

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(G) CELL TYPE: SENESCENT HUMAN CELLS

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(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SENESCENT CELL DERIVED CDNA LIBRARY

(B) CLONE: SDI-1

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGCCGAAG TCAGTTCCTT GTGGAGCCGG AGCTGGGCGC GGATTGCGCG AGGCACCGAG 60
GCACTCAGAG GAGGCGCCAT GTCAGAACCG GCTGGGGATG TCCGTCAGAA CCCATGCGGC 120
AGCAAGGCCT GCCGCCGCCT CTTGCGCCCA GTGGACAGCG AGCAGCTGAG CCGCGACTGT 180
GATGCGCTAA TGGCGGGCTG CATCCAGGAG GCCCCTGAGC GATGGAACCT CGACTTTGTC 240
ACCGAGACAC CACTGGAGGG TGACTTCGCC TGGGAGCGTG TCGGGGGCCT TGGCCTGCCC 300
AAGCTCTACC TTCCACGGG GCCCGGCGA GGCCGGGATG AGTTGGGAGG AGGCAGGCGG 360
CCTGGCACCT CACCTGCTCT GCTGCAGGGG ACAGCAGAGG AAGACCATGT GGACCTGTCA 420
CTGTCTTGTA CCCTTGTCG TCGCTCAGGG GAGCAGGCTG AAGGGTCCCC AGGTGGACCT 480
GGAGACTCTC AGGGTCGAAA ACGGCGGCAG ACCAGCATGA CAGATTCTA CCACTCCAAA 540
CGCCGGCTGA TCTTCTCAA GAGGAAGCCC TAATCCGCC ACAGGAAGCC TGCAGTCCTG 600
GAAGCGGAG GGCCTCAAAG GCCCGCTCTA CATCTTCTG CTTAGTCTCA GTTTGTGTGT 660
CTTAATTATT ATTTGTGTTT TAATTTAAAC ACCTCCTCAT GTACATACCC TGGCCGCCCC 720
CTGCCCCCA GCCTCTGGCA TTAGAATTAT TTAAACAAA ACTAGGCGGT TGAATGAGAG 780
GTTCCTAAGA GTGCTGGGCA TTTTATTTT ATGAAATACT ATTTAAAGCC TCCTCATCCC 840
GTGTTCTCCT TTTCTCTCT CCCGGAGGTT GGGTGGGCG GCTTCATGCC AGCTACTTCC 900
TCCTCCCCAC TTGTCCGCTG GGTGGTACCC TCTGGAGGG TGTGGCTCCT TCCCATCGCT 960
GTCACAGGCG GTTATGAAAT TCACCCCTT TCCTGGACAC TCAGACCTGA ATTCTTTTTC 1020
ATTGAGAAG TAAACAGAT GCACTTTGAA GGGGCCTCAC CGAGTGGGG CATCATCAA 1080
AACTTTGGAG TCCCCTCACC TCCTCTAAGG TTGGGCAGGG TGACCCTGAA GTGAGCACAG 1140
CCTAGGGCTG AGCTGGGGAC CTGGTACCCT CCTGGCTCTT GATACCCCC TCTGTCTTGT 1200
GAAGGCAGGG GGAAGGTGGG GTCCTGGAGC AGACCACCC GCCTGCCCTC ATGGCCCTC 1260
TGACCTGCAC TGGGGAGCCC GTCTCAGTGT TGAGCCTTTT CCCTCTTTGG CTCCCCTGTA 1320
CCTTTTGAGG AGCCCCAGCT ACCCTTCTTC TCCAGCTGGG CTCTGCAATT CCCCTCTGCT 1380
GCTGTCCCTC CCCCTTGTC TTTCCCTTCA GTACCCTCTC AGCTCCAGGT GGCTCTGAGG 1440

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TGCCTGTCCC ACCCCACCCC CCAGCTCAAT GGACTGGAAG GGGAAGGGAC ACACAAGAAG 1500
 AAGGGCACCC TAGTTCTACC TCAGGCAGCT CAAGCAGCGA CCGCCCCCTC CTCTAGCTGT 1560
 5 GGGGGTGAGG GTCCCATGTG GTGGCACAGG CCCCCTTGAG TGGGGTTATC TCTGTGTTAG 1620
 GGGTATATGA TGGGGGAGTA GATCTTTCTA GGAGGGAGAC ACTGGCCCCCT CAAATCGTCC 1680
 10 AGCGACCTTC CTCATCCACC CCATCCCTCC CCAGTTCATT GCACTTTGAT TAGCAGCGGA 1740
 ACAAGGAGTC AGACATTTTA AGATGGTGGC AGTAGAGGCT ATGGACAGGG CATGCCACGT 1800
 GGGCTCATAT GGGGCTGGGA GTAGTTGTCT TTCCTGGCAC TAACGTTGAG CCCCTGGAGG 1860
 15 CACTGAAGTG CTTAGTGTA CTTGAGTATT GGGGTCTGAC CCCAAACACC TTCCAGCTCC 1920
 TGTAACATAC TGGCCTGGAC TGTTTTCTCT CGGCTCCCCA TGTGTCCTGG TTCCCGTTTC 1980
 20 TCCACCTAGA CTGTAAACCT CTCGAGGGCA GGGACCACAC CCTGTACTGT TCTGTGTCTT 2040
 TCACAGCTCC TCCCACAATG CTGATATACA GCAGGTGCTC AATAAACGAT TCTTAGTGAA 2100
 AAAAAA 2106

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

- 35 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS
 40 (B) STRAIN: SDI-1

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Senescent cell derived cDNA library

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys
 1 5 10 15
 50 Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg
 20 25 30

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Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg
 35 40 45

5 Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala
 50 55 60

Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr
 65 70 75 80

10 Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly
 85 90 95

Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp
 100 105 110

15 Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu
 115 120 125

Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln
 130 135 140

20 Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser
 145 150 155 160

25 Lys Arg Lys Pro

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

40 (iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: HOMO SAPIENS

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCCGGTTCT GACATGCCG

19

50 (2) INFORMATION FOR SEQ ID NO:4:

1000960.120701

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: [His]6 leader peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Gly Ser His His His His His His Gly Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Schistosoma japonicum

(vii) IMMEDIATE SOURCE:

(B) CLONE: GST

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 ATGTCCCCTA TACTAGGTTA TTGGAATAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60
 TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTGTATG AGCGCGATGA AGGTGATAAA 120
 TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180
 10 GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAAC 240
 ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCOA TGCTTGAAGG AGCGGTTTTG 300
 15 GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360
 GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTTCG AAGATCGTTT ATGTCATAAA 420
 ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT 480
 20 GTTGTTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTTAAA 540
 AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA 600
 25 TGGCCTTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660
 CTGGTTCCGC GTGGATCCCC GGGAATTCAT CGTGACTGA 699

(2) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 40 (A) ORGANISM: Schistosoma japonicum
- (vii) IMMEDIATE SOURCE:
 (B) CLONE: GST

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15

50 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 5 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 10 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 15 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 20 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 25 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 30 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 35 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Gly Ile His Arg Asp
 225 230

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker fragment for GST-SDI-1 gene fusion

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCCCC GCC

13

(2) INFORMATION FOR SEQ ID NO:8:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker fragment for GST-SDI-1 gene fusion

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCTCGAGGG

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30 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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(v) FRAGMENT TYPE: internal

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(B) CLONE: hinge region of GST-SDI-1 fusion protein

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1194 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GST-SDI-1 gene fusion

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

30

ATGTCCCCTA TACTAGGTTA TTGGAAAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60

TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTTGTATG AGCGCGATGA AGGTGATAAA 120

TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180

35

GGTGAAGTAA AATTAAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAAC 240

ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCAA TGCTTGAAGG AGCGGTTTTG 300

GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

40

GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTG AAGATCGTTT ATGTCATAAA 420

ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT 480

45

GTGTGTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTTTAA 540

AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GSTATATAGCA 600

TGGCCTTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660

50

CTGGTTCCGC GTGGATCCCC TCGAGGGGAT CCCCCGCCA TGTCAGAACC GGCTGGGGAT 720

GTCCGTCAGA ACCCATGCGG CAGCAAGGCC TGCCGCCGCC TCTTCGGCCC AGTGGACAGC 780

5 GAGCAGCTGA GCCGCGACTG TGATGCGCTA ATGGCGGGCT GCATCCAGGA GGCCCGTGAG 840
 CGATGGAACT TCGACTTTGT CACCGAGACA CCACTGGAGG GTGACTTCGC CTGGGAGCGT 900
 GTGCGGGGCC TTGGCCTGCC CAAGCTCTAC CTTCCACGG GGGCCCGGCG AGGCCGGGAT 960
 GAGTTGGGAG GAGGCAGGCG GCCTGGCACC TCACCTGCTC TGCTGCAGGG GACAGCAGAG 1020
 10 GAAGACCATG TGGACCTGTC ACTGTCTTGT ACCCTTGTGC CTCGCTCAGG GGAGCAGGCT 1080
 GAAGGGTCCC CAGGTGGACC TGGAGACTCT CAGGGTCGAA AACGGCGGCA GACCAGCATG 1140
 ACAGATTCTT ACCACTCCAA ACGCCGGCTG ATCTTCTCCA AGAGGAAGCC CTAA 1194
 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 397 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GST-SDI-1 fusion protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
 1 5 10 15
 35 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 40 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 45 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 50 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

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	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
	130						135					140					
5	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
	145					150					155					160	
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
					165					170					175		
10	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	
				180					185					190			
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
15			195					200					205				
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210						215					220					
20	Gly	Ser	Pro	Arg	Gly	Asp	Pro	Pro	Ala	Met	Ser	Glu	Pro	Ala	Gly	Asp	
	225					230					235					240	
	Val	Arg	Gln	Asn	Pro	Cys	Gly	Ser	Lys	Ala	Cys	Arg	Arg	Leu	Phe	Gly	
					245					250					255		
25	Pro	Val	Asp	Ser	Glu	Gln	Leu	Ser	Arg	Asp	Cys	Asp	Ala	Leu	Met	Ala	
				260					265					270			
	Gly	Cys	Ile	Gln	Glu	Ala	Arg	Glu	Arg	Trp	Asn	Phe	Asp	Phe	Val	Thr	
30			275					280					285				
	Glu	Thr	Pro	Leu	Glu	Gly	Asp	Phe	Ala	Trp	Glu	Arg	Val	Arg	Gly	Leu	
	290						295					300					
35	Gly	Leu	Pro	Lys	Leu	Tyr	Leu	Pro	Thr	Gly	Pro	Arg	Arg	Gly	Arg	Asp	
	305					310					315					320	
	Glu	Leu	Gly	Gly	Gly	Arg	Arg	Pro	Gly	Thr	Ser	Pro	Ala	Leu	Leu	Gln	
					325					330					335		
40	Gly	Thr	Ala	Glu	Glu	Asp	His	Val	Asp	Leu	Ser	Leu	Ser	Cys	Thr	Leu	
			340						345					350			
	Val	Pro	Arg	Ser	Gly	Glu	Gln	Ala	Glu	Gly	Ser	Pro	Gly	Gly	Pro	Gly	
45			355					360					365				
	Asp	Ser	Gln	Gly	Arg	Lys	Arg	Arg	Gln	Thr	Ser	Met	Thr	Asp	Phe	Tyr	
	370						375					380					
50	His	Ser	Lys	Arg	Arg	Leu	Ile	Phe	Ser	Lys	Arg	Lys	Pro				
	385					390					395						

(2) INFORMATION FOR SEQ ID NO:12:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs

1000660-120701

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer 12614

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGAGGATCCA TGTCAGAACC GGCT

24

(2) INFORMATION FOR SEQ ID NO:13:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer 12615

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GCAGAATTCC TGTGGGCGGA TTAG

24

40 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

1000990-12071

5 (ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

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15

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20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

30 (iv) ANTI-SENSE: NO

35

TAGGAATTCA CTAGTCTAAG CGTAATCTGG AACATCGTAT GGGTAGGGCT TCCTCTTGGG

60

40 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15

TTCGGCCCTC GAGGCCTGAG CCGCGACTGT

30

(2) INFORMATION FOR SEQ ID NO:17:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTCAGGCCT CGAGGGCCGA AGAAGCGGCG

30

(2) INFORMATION FOR SEQ ID NO:18:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid

1000660-120701

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

15

TTAGCGCGCC TCGAGGCTGC TCGCTGTCCA C

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35

CGAGCAGCCT CGAGGCGCGC TAATGGCGGG C

31

(2) INFORMATION FOR SEQ ID NO:20:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCTGCCCTC GAGGCCGATG GAACTTCGAC

30

15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 CCATCGGCCT CGAGGGCAGC CCGCCATTAG

30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

1000950-120701

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

5

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTGAGCGAC CCCGGGGCGT CACCGAGACA CCACTG

36

15 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

30 (B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCGGTGACG CCCCGGGGTC GCTCAGGGC CTCCTG

36

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

1000660.120701

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCGACCCCTC GAGGCCTGGA GGGTGACTTC

30

(2) INFORMATION FOR SEQ ID NO:25:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCCAGGCCT CGAGGGTCGA AGTTCCATCG

30

35 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

1000960.120701

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10

ACCGAGACAT CCCGGGCCGA CTCGCCTGG GAGCGT

36

(2) INFORMATION FOR SEQ ID NO:27:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GGCGAAGTCG GCCCGGGATG TCTCGGTGAC AAAGTC

36

(2) INFORMATION FOR SEQ ID NO:28:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

1000960-120701

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

10 CCACTGGAGC CCCGGGGCCG TGTGCGGGC CTTGGC

36

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (vii) IMMEDIATE SOURCE:
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

30 CCGCACACGG CCCCGGGGCT CCA GTGGTGT CTCGGT

36

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

1000950-120701

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

5 (B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCTGGCCTC GAGGCGGCCT GCCCAAGCTC

30

10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGCCGCCT CGAGGCCAGG CGAAGTCACC

30

30

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

TOP SECRET 000000

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGGGGCCTTC CCCGGGGCCT TCCACGGGG CCCCGGCGAG G

41

10 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

15 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

25 (B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGTGGGAAGG CCCCAGGGAA GGCCCCGCAC ACGCTCCCAG

40

30

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: internal

TO/03T"0962000T

(vii) IMMEDIATE SOURCE:

(B) CLONE: peptide mimetic fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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Trp Asn Phe Asp Phe Xaa Xaa Xaa Xaa Pro Leu Glu Gly Xaa Xaa Xaa
1 5 10 15

10

Trp Xaa Xaa Val Xaa Xaa Xaa Xaa Leu Pro Xaa Xaa Tyr
20 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

30

CAGAATCACA AGCCACTCGA GGGTAAGTAC GAGTGGGAGC GTGTGCGGGG CCTT

54

(2) INFORMATION FOR SEQ ID NO:36:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

10006660.120701

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTACCCTCG AGTGGCTTGT GATTCTGAAA GTCGAAGTTC CATCGCTC

48

[illegible]